

(1) GENERAL INFORMATION

- (2) INFORMATION FOR SEQ ID NO:1:

- 53

PF-0181 US

Met Leu Ala Arg Ala Ala Arg Gly His Trp Gly Pro Phe Ala Glu Gly
 1 5 10 15
 Leu Ser Thr Gly Phe Trp Pro Arg Ser Gly Arg Ala Ser Ser Gly Leu
 20 25 30
 Pro Arg Asn Thr Val Val Leu Phe Val Pro Gln Gln Glu Ala Trp Val
 35 40 45
 Val Glu Arg Met Gly Arg Phe His Arg Ile Leu Glu Pro Gly Leu Asn
 50 55 60
 Ile Leu Ile Pro Val Leu Asp Arg Ile Arg Tyr Val Gln Ser Leu Lys
 65 70 75 80
 Glu Ile Val Ile Asn Val Pro Glu Gln Ser Ala Val Thr Leu Asp Asn
 85 90 95
 Val Thr Leu Gln Ile Asp Gly Val Leu Tyr Leu Arg Ile Met Asp Pro
 100 105 110
 Tyr Lys Ala Ser Tyr Gly Val Glu Asp Pro Glu Tyr Ala Val Thr Gln
 115 120 125
 Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Leu Ser Xaa Asp
 130 135 140
 Lys Val Phe Arg Glu Arg Glu Ser Leu Asn Ala Ser Ile Val Asp Ala
 145 150 155 160
 Ile Asn Gln Ala Ala Asp Cys Trp Gly Ile Arg Cys Leu Arg Tyr Glu
 165 170 175
 Ile Lys Asp Ile His Val Pro Pro Arg Val Lys Glu Ser Met Gln Met
 180 185 190
 Gln Val Glu Ala Glu Arg Arg Lys Arg Ala Thr Val Leu Glu Ser Glu
 195 200 205
 Gly Thr Arg Glu Ser Ala Ile Asn Val Ala Glu Gly Lys Lys Gln Ala
 210 215 220
 Gln Ile Leu Ala Ser Glu Ala Glu Lys Ala Glu Gln Ile Asn Gln Ala
 225 230 235 240
 Ala Gly Glu Ala Ser Ala Val Leu Ala Lys Ala Lys Ala Lys Ala Glu
 245 250 255
 Ala Ile Arg Ile Leu Ala Ala Ala Leu Thr Gln His Asn Gly Asp Ala
 260 265 270
 Ala Ala Ser Leu Thr Val Ala Glu Gln Tyr Val Ser Ala Phe Ser Lys
 275 280 285
 Leu Ala Lys Asp Ser Asn Thr Ile Leu Leu Pro Ser Asn Pro Gly Asp
 290 295 300
 Val Thr Ser Met Val Ala Gln Ala Met Gly Val Tyr Gly Ala Leu Thr
 305 310 315 320
 Lys Ala Pro Val Pro Gly Thr Pro Asp Ser Leu Ser Ser Gly Ser Ser
 325 330 335
 Arg Asp Val Gln Gly Thr Asp Ala Ser Xaa Asp Glu Glu Leu Asp Arg
 340 345 350
 Val Lys Met Ser
 355

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTTCTGGG	AGCNACCGCT	CCGCTCGTCT	CGTTGGTTCC	GGAGGTGCT	GCGGCGGTGG	60
GAAATGCTGG	CGCGCGCGGC	GCGGGGGCAC	TGGGGCCCTT	TTGCTGAGGG	GCTCTCTACT	120
GGCTTCTGGC	CGCGCTCCGG	CCGCGCCTCC	TCTGGATTGC	CCC3AAACAC	CGTGGTACTG	180
TTGCTGCCGC	AGCAGGAGGC	CTGGGTGGTG	GAGCGAATGG	GCCGATTCCA	CCGGATCCTG	240
GAGCCTGGTT	TGAACATCCT	CATCCCTGTG	TTAGACCGGA	TCCGATATGT	GCAGAGTCTC	300
AAGGAAATTG	TCATCAACGT	GCCTGAGCAG	TCGGCTGTGA	CTCTCGACAA	TGTAACCTCTG	360
CAATCGATG	GAGTCCTTTA	CCTGCGCATC	ATGGACCCTT	ACAAGGCAAG	CTACGGTGTG	420
GAGGACCCTG	AGTATGCCGT	CACCCAGCTA	GCTCAAACAA	CCATGAGATC	AGAGCTCGGC	480
AAACTCTCTN	TGGACAAAGT	CTTCCGGGAA	CGGGAGTCCC	TGAATGCCAG	CATTGTGGAT	540
GCCATCAACC	AAGCTGCTGA	CTGCTGGGGT	ATCCGCTGCC	TNCGTTATGA	GATCAAGGAT	600
ATCCATGTGC	CACCCCGGGT	GAAAGAGTCT	ATGCAGATGC	AGGTGGAGGC	AGAGCGGCGG	660
AAACGGGCCA	CAGTTCTAGA	GTCTGAGGGG	ACCCGAGAGT	CGGCCATCAA	TGTGGCAGAA	720
GGGAAGAAAC	AGGCCCAGAT	CCTGGCCTCC	GAAGCAGAAA	AGGCTGAACA	GATAAATCAG	780
GCAGCAGGAG	AGGCCAGTGC	AGTTCTGGCG	AAGGCCAAGG	CTAAAGCTGA	AGCTATTCTGA	840
ATCCTGGCTG	CAGCTCTGAC	ACAACATAAT	GGAGATGCAG	CAGCTTCACT	GACTGTGGCC	900
GAGCAGTATG	TCAGCGCGTT	CTCCAAACTG	GCCAAGGACT	CCAACACTAT	CCTACTGCCC	960
TCCAACCCTG	GCGATGTAC	CAGCATGGTG	GCTCAGGCCA	TGGGTGTATA	TGGAGCCCTC	1020
ACCAAAGCCC	CAGTGCCAGG	GACTCCAGAC	TCACTCTCCA	GTGGGAGCAG	CAGAGATGTC	1080
CAGGGTACAG	ATGCAAGTNT	TGATGAGGAA	CTTGATCGAG	TCAAGATGAG	TTAGTGGAGC	1140
TGGGCTTNGC	CAGGGAGTCT	GGGACAAGG	AAGCAGATTT	TCCTGATT		1188

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genbank
- (B) CLONE: 31069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Glu	Lys	Arg	His	Thr	Arg	Asp	Ser	Glu	Ala	Gln	Arg	Leu	Pro
1				5					10					15	
Asp	Ser	Phe	Lys	Asp	Ser	Pro	Ser	Lys	Gly	Leu	Gly	Pro	Cys	Gly	Trp
			20					25					30		
Ile	Leu	Val	Ala	Phe	Ser	Phe	Leu	Phe	Thr	Val	Ile	Thr	Phe	Pro	Ile
		35					40					45			
Ser	Ile	Trp	Met	Cys	Ile	Lys	Ile	Ile	Lys	Glu	Tyr	Glu	Arg	Ala	Ile
	50				55					60					
Ile	Phe	Arg	Leu	Gly	Arg	Ile	Leu	Gln	Gly	Gly	Ala	Lys	Gly	Pro	Gly
65				70					75					80	
Leu	Phe	Phe	Ile	Leu	Pro	Cys	Thr	Asp	Ser	Phe	Ile	Lys	Val	Asp	Met
			85					90						95	
Arg	Thr	Ile	Ser	Phe	Asp	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Lys	Asp
			100					105					110		
Ser	Val	Thr	Ile	Ser	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Val	Gln	Asn
		115					120					125			
Ala	Thr	Leu	Ala	Val	Ala	Asn	Ile	Thr	Asn	Ala	Asp	Ser	Ala	Thr	Arg
	130					135					140				
Leu	Leu	Ala	Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Lys	Asn	Leu
145				150					155					160	
Ser	Gln	Ile	Leu	Ser	Asp	Arg	Glu	Glu	Ile	Ala	His	Asn	Met	Gln	Ser
			165					170						175	
Thr	Leu	Asp	Asp	Ala	Thr	Asp	Ala	Trp	Gly	Ile	Lys	Val	Glu	Arg	Val
		180					185						190		
Glu	Ile	Lys	Asp	Val	Lys	Leu	Pro	Val	Gln	Leu	Gln	Arg	Ala	Met	Ala
	195					200						205			

Ala	Glu	Ala	Glu	Ala	Ser	Arg	Glu	Ala	Arg	Ala	Lys	Val	Ile	Ala	Ala
210						215					220				
Glu	Gly	Glu	Met	Asn	Ala	Ser	Arg	Ala	Leu	Lys	Glu	Ala	Ser	Met	Val
225					230					235					240
Ile	Thr	Glu	Ser	Pro	Ala	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu
				245					250					255	
Thr	Thr	Ile	Ala	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	
			260				265						270		
Ile	Asp	Met	Leu	Gln	Gly	Ile	Ile	Gly	Ala	Lys	His	Ser	His	Leu	Gly
	275						280						285		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1065452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asn	Leu	Lys	Thr	Cys	Ser	Leu	Ser	Thr	His	Ser	Phe	Leu	Gln	Lys
1				5					10					15	
Lys	Asn	Glu	Lys	His	Asp	Gly	Asn	Pro	Glu	His	Tyr	Asp	Thr	Gly	Leu
			20					25					30		
Gly	Phe	Cys	Gly	Trp	Phe	Leu	Met	Gly	Leu	Ser	Trp	Ile	Met	Val	Ile
		35					40					45			
Ser	Thr	Phe	Pro	Val	Ser	Ile	Tyr	Phe	Cys	Met	Lys	Val	Val	Gln	Glu
	50					55					60				
Tyr	Glu	Arg	Ala	Val	Ile	Phe	Arg	Leu	Gly	Arg	Leu	Ile	Gly	Gly	Gly
65					70					75					80
Ala	Lys	Gly	Pro	Gly	Ile	Phe	Phe	Val	Leu	Pro	Cys	Ile	Glu	Ser	Tyr
				85					90					95	
Thr	Lys	Val	Asp	Leu	Arg	Thr	Val	Ser	Phe	Ser	Val	Pro	Pro	Gln	Glu
			100					105					110		
Ile	Leu	Thr	Lys	Asp	Ser	Val	Thr	Ser	Val	Asp	Ala	Val	Ile	Tyr	
		115					120				125				
Tyr	Arg	Ile	Ser	Asn	Ala	Thr	Val	Ser	Val	Ala	Asn	Val	Glu	Asn	Ala
	130					135					140				
His	His	Ser	Thr	Arg	Leu	Ala	Gln	Thr	Thr	Leu	Arg	Asn	Met	Leu	
145					150					155				160	
Gly	Thr	Arg	Ser	Leu	Ser	Glu	Ile	Leu	Ser	Asp	Arg	Glu	Thr	Leu	Ala
				165					170					175	
Ala	Ser	Met	Gln	Thr	Ile	Leu	Asp	Glu	Ala	Thr	Glu	Ser	Trp	Gly	Ile
			180					185					190		
Lys	Val	Glu	Arg	Val	Glu	Ile	Lys	Asp	Val	Arg	Leu	Pro	Ile	Gln	Leu
		195					200					205			
Gln	Arg	Ala	Met	Ala	Ala	Glu	Ala	Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala
	210					215					220				
Lys	Val	Ile	Ala	Ala	Glu	Gly	Glu	Gln	Lys	Ala	Ser	Arg	Ala	Leu	Arg
225					230					235					240
Asp	Ala	Ala	Ser	Val	Ile	Ala	Gln	Ser	Pro	Ala	Ala	Leu	Gln	Leu	Arg
				245					250					255	
Tyr	Leu	Gln	Thr	Leu	Asn	Ser	Val	Ala	Arg	Glu	Lys	Phe	Asp	Asp	His
			260					265					270		
Leu	Pro	Thr	Ser	Asp	Gly	Ile	Ser								
		275					280								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1353669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Tyr Gly Met Pro Glu Gly Ser Tyr Asp Ser Val Phe Thr Tyr
 1 5 10 15
 Ala Pro Tyr Asn Asp Leu Asp Lys Met Gly Tyr Met Gly Pro Ala Arg
 20 25 30
 Gln Gly Met Met Leu Gly Asn Lys Tyr Gly Asn Phe Thr Tyr Thr Arg
 35 40 45
 Asp Tyr Gly Val Asn Met Glu Asp Asp Ile Lys Pro Leu Ser Ala Ile
 50 55 60
 Glu Leu Leu Ile Phe Cys Val Ser Phe Leu Phe Val Val Met Thr Met
 65 70 75 80
 Pro Leu Ser Leu Leu Phe Ala Leu Lys Phe Ile Ser Thr Ser Glu Lys
 85 90 95
 Leu Val Val Leu Arg Leu Gly Arg Ala Gln Lys Thr Arg Gly Pro Gly
 100 105 110
 Ile Thr Leu Val Ile Pro Cys Ile Asp Thr Thr His Lys Val Thr Met
 115 120 125
 Ser Ile Thr Ala Phe Asn Val Pro Pro Leu Gln Ile Ile Thr Thr Asp
 130 135 140
 Arg Gly Leu Val Glu Leu Gly Ala Thr Val Phe Leu Lys Ile Arg Asp
 145 150 155 160
 Pro Ile Ala Ala Val Cys Gly Val Gln Asp Arg Asn Ala Ser Val Arg
 165 170 175
 Thr Leu Ala Asn Thr Met Leu Tyr Arg Tyr Ile Ser Lys Lys Arg Ile
 180 185 190
 Cys Asp Val Thr Ser Ser Gln Asp Arg Arg Ile Ile Ser Ala Asn Leu
 195 200 205
 Lys Asp Glu Leu Gly Ser Phe Thr Cys Gln Phe Gly Val Glu Ile Thr
 210 215 220
 Asp Val Glu Ile Ser Asp Val Lys Ile Val Lys Glu Gly Glu Asn Met
 225 230 235 240
 Gly Met Ser Ala Leu Ser Ser Val Ala Lys Ser Asp Ala Gly Gln Gln
 245 250 255
 Leu Trp Gln Val Ile Gly Pro Val Phe Glu Asp Phe Ala Lys Glu Cys
 260 265 270
 Ala Ala Glu Glu Lys Ala Lys Glu Asn Ala Pro Leu Val Asp Leu Ser
 275 280 285
 Asp Val Pro Ser Thr Ser Ala Ala Gly Thr Ser Thr Asp Thr Pro Asn
 290 295 300
 Ile Pro Ser Ile Asp Ile Asp His Leu Ile Ser Val Ala Ser Leu Ala
 305 310 315 320
 Met Asp Glu His Leu Val Arg Leu Ile Gly Arg Val Phe Gln Ile Asn
 325 330 335
 Cys Lys Asp Ile Glu Pro Ile Cys Ile Asp Leu Lys His Gly Ser Gly
 340 345 350
 Ser Ala Tyr Lys Gly Thr Ser Leu Asn Pro Asp Val Val Phe Glu Thr
 355 360 365
 Ser Leu Glu Val Phe Gly Lys Ile Leu Thr Lys Glu Val Ser Pro Val

370 375 380
 Thr Val Tyr Met Asn Gly Asn Leu Lys Val Lys Gly Ser Ile Gln Asp
 385 390 395 400
 Ala Met Gln Leu Lys His Leu Val Glu Arg Met Ser Asp Trp Leu
 405 410 415

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Owl
 (B) CLONE: 79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Gly Ala Val Ala Gly Leu Val Phe Leu Ala Val Leu Val Ile
 1 5 10 15
 Phe Ala Ile Ile Val Val Ala Lys Ser Val Ala Leu Ile Pro Gln Ala
 20 25 30
 Glu Ala Ala Val Ile Glu Arg Leu Gly Arg Tyr Ser Arg Thr Val Ser
 35 40 45
 Gly Gln Leu Thr Leu Leu Val Pro Phe Ile Asp Arg Val Arg Ala Arg
 50 55 60
 Val Asp Leu Arg Glu Arg Val Val Ser Phe Pro Gln Pro Val Ile
 65 70 75 80
 Thr Glu Asp Asn Leu Thr Leu Asn Ile Asp Thr Val Val Tyr Phe Gln
 85 90 95
 Val Thr Val Pro Gln Ala Ala Val Tyr Glu Ile Ser Asn Tyr Ile Val
 100 105 110
 Gly Val Glu Gln Leu Thr Thr Thr Leu Arg Asn Val Val Gly Gly
 115 120 125
 Met Thr Leu Glu Gln Thr Leu Thr Ser Arg Asp Gln Ile Asn Ala Gln
 130 135 140
 Leu Arg Gly Val Leu Asp Glu Ala Thr Gly Arg Trp Gly Leu Arg Val
 145 150 155 160
 Ala Arg Val Glu Leu Arg Ser Ile Asp Pro Pro Pro Ser Ile Gln Ala
 165 170 175
 Ser Met Glu Lys Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Met Ile
 180 185 190
 Leu Thr Ala Glu Gly Thr Arg Glu Ala Ala Ile Lys Gln Ala Glu Gly
 195 200 205
 Gln Lys Gln Ala Gln Ile Leu Ala Ala Glu Gly Ala Lys Gln Ala Ala
 210 215 220
 Ile Leu Ala Ala Glu Ala Asp Arg Gln Ser Arg Met Leu Arg Ala Gln
 225 230 235 240
 Gly Glu Arg Ala Ala Tyr Leu Gln Ala Gln Gly Gln Ala Lys Ala
 245 250 255
 Ile Glu Lys Thr Phe Ala Ala Ile Lys Ala Gly Arg Pro Thr Pro Glu
 260 265 270
 Met Leu Ala Tyr Gln Tyr Leu Gln Thr Leu Pro Glu Met Ala Arg Gly
 275 280 285
 Asp Ala Asn Lys Val Trp Val Val Pro Ser Asp Phe Asn Ala Ala Leu
 290 295 300
 Gln Gly Phe Thr Arg Leu Leu Gly Lys Pro Gly Glu Asp Gly Val Phe
 305 310 315 320
 Arg Phe Glu Pro Ser Pro Val Glu Asp Gln Pro Lys His Ala Ala Asp

				325						330						335
Gly	Asp	Asp	Ala	Glu	Val	Ala	Gly	Trp	Phe	Ser	Thr	Asp	Thr	Asp	Pro	
			340					345					350			
Ser	Ile	Ala	Arg	Ala	Val	Ala	Thr	Ala	Glu	Ala	Ile	Ala	Arg	Lys	Pro	
		355					360					365				
Val	Glu	Gly	Ser	Leu	Gly	Thr	Pro	Pro	Arg	Leu	Thr	Gln				
	370					375					380					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1591514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Lys	Val	Asn	Asp	Met	Phe	Trp	Phe	Trp	Leu	Ile	Leu	Gly	Ile	Ile
1				5					10					15	
Ala	Leu	Phe	Ile	Ile	Val	Lys	Ala	Ile	Val	Ile	Val	Asn	Gln	Tyr	Glu
			20					25					30		
Gly	Gly	Leu	Ile	Phe	Arg	Leu	Gly	Arg	Val	Ile	Gly	Lys	Leu	Lys	Pro
		35					40					45			
Gly	Ile	Asn	Ile	Ile	Ile	Pro	Phe	Leu	Asp	Val	Pro	Val	Lys	Val	Asp
	50					55					60				
Met	Arg	Thr	Arg	Val	Thr	Asp	Ile	Pro	Pro	Gln	Glu	Met	Ile	Thr	Lys
65					70					75				80	
Asp	Asn	Ala	Val	Val	Lys	Val	Asp	Ala	Val	Val	Tyr	Tyr	Arg	Val	Ile
			85						90					95	
Asp	Val	Glu	Lys	Ala	Ile	Leu	Glu	Val	Glu	Asp	Tyr	Glu	Tyr	Ala	Ile
			100					105					110		
Ile	Asn	Leu	Ala	Gln	Thr	Thr	Leu	Arg	Ala	Ile	Ile	Gly	Ser	Met	Glu
	115						120					125			
Leu	Asp	Glu	Val	Leu	Asn	Lys	Arg	Glu	Tyr	Ile	Asn	Ser	Lys	Leu	Leu
	130					135					140				
Glu	Ile	Leu	Asp	Arg	Glu	Thr	Asp	Ala	Trp	Gly	Val	Arg	Ile	Glu	Lys
145					150					155				160	
Val	Glu	Val	Lys	Glu	Ile	Asp	Pro	Pro	Glu	Asp	Ile	Lys	Asn	Ala	Met
			165						170					175	
Ala	Gln	Gln	Met	Lys	Ala	Glu	Arg	Leu	Lys	Arg	Ala	Ala	Ile	Leu	Glu
			180					185						190	
Ala	Glu	Gly	Glu	Lys	Pro	Glu									
	195														